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- 1 -

SEQUENCE LISTING

<110> THE CORPORATION OF THE TRUSTEES OF THE ORDER OF THE SISTERS OF
MERCY IN QUEENSLAND

<120> NOVEL THERAPEUTIC MOLECULES AND USES THEREOF

<130> 12381870/TDO

<150> 2002953223

<151> 2002-06-12

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 5622

<212> DNA

<213> mammalian

<220>

<221> CDS

<222> (1)..(5619)

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Val Glu Gly Thr Leu Cys Lys	Thr Ala Ile Pro Tyr	Lys Arg Lys	
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Tyr Leu Ser Asp Asn His Ile	Leu Ile Ser Ala Leu	Val Ile Ala	
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Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
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His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
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His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
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Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
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Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
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Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
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Pro	Asp	Trp	Tyr	Asn	Pro	Asp	Arg	Ala	Gly	Ile	His	Gly	Pro	Pro	Leu	805	810	815	
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Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
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Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
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Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
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Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu
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His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr
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Ala Leu Pro Ala Leu Leu Leu Pro Leu Leu Gly Leu Ala Ala Ala Ala
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gtc gcg gac tgt cct tca tct act tgg att cag ttc caa gac agt tgt 152
Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe Gln Asp Ser Cys
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tac att ttt ctc caa gaa gcc atc aaa gta gaa agc ata gag gat gtc 200
Tyr Ile Phe Leu Gln Glu Ala Ile Lys Val Glu Ser Ile Glu Asp Val
          40          45          50

aga aat cag tgt act gac cat gga gcg gac atg ata agc ata cat aat 248
Arg Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile Ser Ile His Asn
          55          60          65

gaa gaa gaa aat gct ttt ata ctg gat act ttg aaa aag caa tgg aaa 296

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[illegible]

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Ala Ala Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
20          25          30

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Gln Asp Ser Cys Tyr Ile Phe Leu Gln Glu Ala Ile Lys Val Glu Ser
35          40          45

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```

Ile Glu Asp Val Arg Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile
50          55          60

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Ser Ile His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Lys
65          70          75          80

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Lys Gln Trp Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp
85 90 95

Thr Asp Asp Ala Ser Phe Lys Trp Phe Asp Asn Ser Asn Met Thr Phe
100 105 110

Asp Lys Trp Thr Asp Gln Asp Asp Glu Asp Leu Val Asp Thr Cys
115 120 125

Ala Phe Leu His Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys Glu
130 135 140

Val Ser Ser Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro Tyr Lys
145 150 155 160

Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala Leu Val Ile
165 170 175

Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile Ile Trp Phe Leu
180 185 190

Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr Val Phe Ser Thr Ala
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3740

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gtc atg ccc cac gca gcg ctg tcc tcg ctc gtg ctg ctg agc ctc gcc 408
Met Pro His Ala Ala Leu Ser Ser Leu Val Leu Leu Ser Leu Ala
1 5 10 15
act gcc atc gtc gcc gac tgt cct tca tct acc tgg gtc cag ttc caa 456
Thr Ala Ile Val Ala Asp Cys Pro Ser Ser Thr Trp Val Gln Phe Gln
20 25 30
ggc agc tgt tat gct ttt ctt caa gta acc atc aat gtg gaa aac ata 504
Gly Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile
35 40 45
gag gat gtc aga aaa cag tgc act gac cac ggg gca gac atg gta agc 552
Glu Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser
50 55 60
ata cac aat gaa gag gaa aac gcg ttt ata ctg gac act ttg caa aag 600
Ile His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys
65 70 75
cga tgg aag ggt cca gat gat ctc ctg cta ggc atg ttc tat gac act 648
Arg Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr
80 85 90 95
gat gat gca act ttc aag tgg tat gat cat tca aat atg aca ttc gac 696
Asp Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp
100 105 110

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Lys Trp Ala Asp Gln Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe	
115 120 125	
ctg tac acc aag aca ggt gaa tgg aga aaa ggg gat tgt gaa atc tct	792
Leu Tyr Thr Lys Thr Gly Glu Trp Arg Lys Gly Asp Cys Glu Ile Ser	
130 135 140	
tct gtg gag gga aca ctt tgc aaa gca gca atc cca tat gac aag aag	840
Ser Val Glu Gly Thr Leu Cys Lys Ala Ala Ile Pro Tyr Asp Lys Lys	
145 150 155	
tat tta tca gat aac cac att tta ata tgc act ctg gtg atc gct agc	888
Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser	
160 165 170 175	
aca gta act ctg gca gtt ttg gga gcg atc att tgg ttc ctc tat aga	936
Thr Val Thr Leu Ala Val Leu Gly Ala Ile Ile Trp Phe Leu Tyr Arg	
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aga aac gcg cgc tct ggc ttc acc tct ttt tca cct gca cca ctg tca	984
Arg Asn Ala Arg Ser Gly Phe Thr Ser Phe Ser Pro Ala Pro Leu Ser	
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Pro Tyr Ser Asp Gly Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr	
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Ala Val Gln Leu Asp	
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20 25 30

Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu
35 40 45

Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser Ile
50 55 60

His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg
65 70 75 80

Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp
85 90 95

Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp Lys
100 105 110

Trp Ala Asp Gln Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu
115 120 125

Tyr Thr Lys Thr Gly Glu Trp Arg Lys Gly Asp Cys Glu Ile Ser Ser
130 135 140

Val Glu Gly Thr Leu Cys Lys Ala Ala Ile Pro Tyr Asp Lys Lys Tyr
145 150 155 160

Leu Ser Asp Asn His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr
165 170 175

Val Thr Leu Ala Val Leu Gly Ala Ile Ile Trp Phe Leu Tyr Arg Arg
180 185 190

Asn Ala Arg Ser Gly Phe Thr Ser Phe Ser Pro Ala Pro Leu Ser Pro
195 200 205

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210 215 220

Val Gln Leu Asp
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Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
20 25 30

ttt ctt caa gta acc atc aat gtg gaa aac ata gag gat gtc aga aag 144
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
35 40 45

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cag tgt act gat cac ggg gca gac ctg gta agt ata cac aat gaa gaa	192
Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu	
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Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro	
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gat gat ctt ctg cta ggc atg ttt tat gac act gat gat gca agt ttc	288
Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe	
85 90 95	
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Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu	
100 105 110	
gat ggt gag gac cta gtt gac acc tgt ggt ttt ctg tat gcc aag aca	384
Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr	
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Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr	
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Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn	
145 150 155 160	
cac att tta ata tcg act ctg gtg atc gct agc aca gtg act ctg gca	528
His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala	
165 170 175	
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Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser	
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ggc ttc acc tct ttc tct cct gca cca caa tca cct tac agt gat ggc	624
Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly	
195 200 205	
tgt gct ctg gta gtt gcg gaa gaa gat gaa tac tct gtt cag ctg gac	672
Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp	
210 215 220	
tgagagtttg ggaacatcag acgagcacac tgaacacctt gacaagaaat aatttcctat	732
gcaagattgt catgtaaaat ttgccacgga aaactgaacc ttttatggta ttccttattc	792
ttctaacaat attttcatgt attcaatgtg acaaaacata aaccttctga ttaaaaggaa	852
aaaaagtagg ttccagaaaa ggaactagca cagagctaac ttacaggttt tcttaagtag	912
ttttcatttg agtaaatgaa agctacagta caataaagct ggtaaaacgc aaaaaaaaaa	972
aaaaaaaa	979

<210> 11
 <211> 224
 <212> PRT
 <213> mammalian

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> The 'Xaa' at location 5 stands for Leu.

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> The 'Xaa' at location 13 stands for Ala, or Val.

<220>
 <221> misc_feature
 <222> (142)..(142)
 <223> The 'Xaa' at location 142 stands for Thr.

<400> 11

His	Glu	Ala	Ser	Xaa	Val	Leu	Leu	Ser	Leu	Ala	Thr	Xaa	Ile	Phe	Ala
1				5					10					15	

Asp	Cys	Pro	Ser	Ser	Ile	Trp	Val	Gln	Phe	Gln	Gly	Ser	Cys	Tyr	Thr
			20					25					30		

Phe	Leu	Gln	Val	Thr	Ile	Asn	Val	Glu	Asn	Ile	Glu	Asp	Val	Arg	Lys
		35					40					45			

Gln	Cys	Thr	Asp	His	Gly	Ala	Asp	Leu	Val	Ser	Ile	His	Asn	Glu	Glu
	50					55					60				

Glu	Asn	Ala	Phe	Ile	Leu	Asp	Thr	Leu	Gln	Lys	Arg	Trp	Lys	Gly	Pro
65					70					75					80

Asp	Asp	Leu	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr	Asp	Asp	Ala	Ser	Phe
			85						90					95	

Lys	Trp	Phe	Asp	Gln	Ser	Asn	Met	Thr	Phe	Asp	Lys	Trp	Ala	Asp	Glu
			100					105					110		

Asp	Gly	Glu	Asp	Leu	Val	Asp	Thr	Cys	Gly	Phe	Leu	Tyr	Ala	Lys	Thr
		115					120					125			

Gly	Glu	Trp	Arg	Lys	Gly	Asn	Cys	Glu	Met	Ser	Ser	Val	Xaa	Gly	Thr
		130				135					140				

Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn
145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala
165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser
180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly
195 200 205

Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp
210 215 220

<210> 12
<211> 979
<212> DNA
<213> mammalian

<400> 12
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aggtagaccc aagtcaaggt tccgtcgaca atgtgaaaag aagttcattg gtagttacac 120
cttttgtatc tcctacagtc tttcgtcaca tgactagtgc cccgtctgga ccattcatat 180
gtgttacttc ttcttttgcg taaatatgac ctgtgaaatg ttttcgctac ctttccgggc 240
ctactagaag acgatccgta caaaatactg tgactactac gttcaaagtt caccaaacta 300
gtcagtttat actgtaagct gttcacccgt ctactcctac cactcctgga tcaactgtgg 360
acacccaaaag acatacgggt ctgtccactt acctcttttc ctttaacact ttacagaaga 420
cactgycctt gtgaaacggt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480
gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540
cagtaaacca aggagatata ttctcgcgt gcgagaccga agtggagaaa gagaggacgt 600
gggtgttagtg gaatgtcact accgacacga gaccatcaac gccttcttct acttatgaga 660
caagtcgacc tgactctcaa acccttgtag tctgctcgtg tgacttgtgg aactgttctt 720
tattaaagga tacgttctaa cagtacattt taaacgggtgc cttttgactt ggaaaatacc 780
ataaggaata agaagattgt tataaaagta cataagttac actgttttgt atttggaaga 840
ctaattttcc tttttttcat ccaaagtctt ttcttgcgtc gtgtctcgat tgaatgtcca 900

aaagaattca tcaaaagtaa actcatttac ttctgatgtc atgttatttc gaccattttg 960
cgtttttttt tttttttttt 979

<210> 13
<211> 483
<212> DNA
<213> mammalian

<220>
<221> misc_feature
<222> (43)..(43)
<223> n is any nucleic acid

<400> 13
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ctgtgaagtt tcttctgtgg aaggaaccct ttgtaaagca gctatcccat atgaaaagaa 120
atatttatca gataaccgca ttttaatatc agctttgggtg attgctagca cagtaattct 180
gacagttctg ggagcagttg tttggttctt gtacaaaaga agtttggatt ctggtttcac 240
cacagttttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300
agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360
aatacctttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaaattagt 420
ttttatgata tattacctta ttccagtaac attcattact cttatgtaaa atcactgatc 480
atg 483

<210> 14
<211> 27
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(27)
<223>

<400> 14
aaa gtg cct ctg ggc cct gat tac aca 27
Lys Val Pro Leu Gly Pro Asp Tyr Thr
1 5

<210> 15
<211> 9
<212> PRT
<213> mammalian

<400> 15

Lys Val Pro Leu Gly Pro Asp Tyr Thr
1 5

<210> 16
<211> 42
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(42)
<223>

<400> 16
aaa gtg cct ctg gac tgt cct tca tct act tgg att cag ttc 42
Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 17
<211> 14
<212> PRT
<213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 18
<211> 42
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(42)
<223>

<400> 18
gct gcc gtc gcg gac tgt cct tca tct act tgg att cag ttc 42
Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 19
 <211> 14
 <212> PRT
 <213> mammalian

<400> 19

Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
 1 5 10

<210> 20
 <211> 5454
 <212> DNA
 <213> mammalian

<220>
 <221> CDS
 <222> (1)..(5451)
 <223>

<400> 20

atg agg aca ggc tgg gcg acc cct cgc cgc ccg gcg ggg ctc ctc atg 48
 Met Arg Thr Gly Trp Ala Thr Pro Arg Arg Pro Ala Gly Leu Leu Met
 1 5 10 15

ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct 96
 Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala
 20 25 30

aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag 144
 Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
 35 40 45

cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac 192
 Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
 50 55 60

aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc 240
 Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
 65 70 75 80

caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga 288
 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
 85 90 95

atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac 336
 Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
 100 105 110

cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga 384
 His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
 115 120 125

cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly 130 135 140	432
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg 145 150 155 160	480
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp 165 170 175	528
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro 180 185 190	576
tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile 195 200 205	624
tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu 210 215 220	672
cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp 225 230 235 240	720
aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser 245 250 255	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile 260 265 270	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly 275 280 285	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro 290 295 300	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met 305 310 315 320	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu 325 330 335	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp 340 345 350	1056

gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat	1104
Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn	
355 360 365	
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag	1152
Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys	
370 375 380	
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat	1200
Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His	
385 390 395 400	
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat	1248
Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp	
405 410 415	
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act	1296
Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr	
420 425 430	
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat	1344
Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp	
435 440 445	
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc	1392
Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser	
450 455 460	
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa	1440
Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys	
465 470 475 480	
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt	1488
Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser	
485 490 495	
tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa	1536
Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu	
500 505 510	
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc	1584
Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys	
515 520 525	
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg	1632
Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu	
530 535 540	
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg	1680
Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu	
545 550 555 560	
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga	1728
Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly	
565 570 575	

aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776
Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala	
580 585 590	
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag	1824
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys	
595 600 605	
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872
Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys	
610 615 620	
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat	1920
Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp	
625 630 635 640	
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt	1968
Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys	
645 650 655	
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa	2016
Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu	
660 665 670	
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc	2064
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe	
675 680 685	
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag	2112
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln	
690 695 700	
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca	2160
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro	
705 710 715 720	
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act	2208
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr	
725 730 735	
att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt	2256
Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys	
740 745 750	
gct gct gtc aag gta ttt cat agg cca tgg cga aga ggc tgg cat ttc	2304
Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe	
755 760 765	
tat gat gat aga gaa ttt att tat ttg agg cct ttt gct tgt gat aca	2352
Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr	
770 775 780	
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca	2400
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr	
785 790 795 800	

cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt	2448
Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu	
805 810 815	
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac	2496
Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn	
820 825 830	
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg	2544
Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala	
835 840 845	
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca	2592
Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala	
850 855 860	
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg	2640
Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp	
865 870 875 880	
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt	2688
Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe	
885 890 895	
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg	2736
Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp	
900 905 910	
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc	2784
Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe	
915 920 925	
atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat	2832
Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp	
930 935 940	
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat	2880
Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn	
945 950 955 960	
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca	2928
Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala	
965 970 975	
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc	2976
Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser	
980 985 990	
cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct	3024
Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala	
995 1000 1005	
act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac	3069
Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn	
1010 1015 1020	

aaa tgg aca gat aac aga gag ctg acg tac agt aac ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro	
1025 1030 1035	
tta ttg gtt agt ggg agg ctg aga ata cca gaa aat ttt ttt gag	3159
Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu	
1040 1045 1050	
gaa gag tct cgc tac cac tgt gcc cta ata ctc aac ctc caa aaa	3204
Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys	
1055 1060 1065	
tca ccg ttt act ggg acg tgg aat ttt aca tcc tgc agt gaa cgc	3249
Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg	
1070 1075 1080	
cac ttt gtg tct ctc tgt cag aaa tat tca gaa gtt aaa agc aga	3294
His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg	
1085 1090 1095	
cag acg ttg cag aat gct tca gaa act gta aag tat cta aat aat	3339
Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn	
1100 1105 1110	
ctg tac aaa ata atc cca aag act ctg act tgg cac agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys	
1115 1120 1125	
agg gag tgt ctg aaa agt aac atg cag ctg gtg agc atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp	
1130 1135 1140	
cct tac cag cag gca ttc ctc agt gtg cag gcg ctc ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn	
1145 1150 1155	
tct tcc tta tgg atc gga ctc ttc agt caa gat gat gaa ctc aac	3519
Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn	
1160 1165 1170	
ttt ggt tgg tca gat ggg aaa cgt ctt cat ttt agt cgc tgg gct	3564
Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala	
1175 1180 1185	
gaa act aat ggg caa ctc gaa gac tgt gta gta tta gac act gat	3609
Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp	
1190 1195 1200	
gga ttc tgg aaa aca gtt gat tgc aat gac aat caa cca ggt gct	3654
Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala	
1205 1210 1215	
att tgc tac tat tca gga aat gag act gaa aaa gag gtc aaa cca	3699
Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro	
1220 1225 1230	

gtt gac agt gtt aaa tgt cca tct cct gtt cta aat act ccg tgg	3744
Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp	
1235 1240 1245	
ata cca ttt cag aac tgt tgc tac aat ttc ata ata aca aag aat	3789
Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn	
1250 1255 1260	
agg cat atg gca aca aca cag gat gaa gtt cat act aaa tgc cag	3834
Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln	
1265 1270 1275	
aaa ctg aat cca aaa tca cat att ctg agt att cga gat gaa aag	3879
Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys	
1280 1285 1290	
gag aat aac ttt gtt ctt gag caa ctg ctg tac ttc aat tat atg	3924
Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met	
1295 1300 1305	
gct tca tgg gtc atg tta gga ata act tat aga aat aat tct ctt	3969
Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu	
1310 1315 1320	
atg tgg ttt gat aag acc cca ctg tca tat aca cat tgg aga gca	4014
Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala	
1325 1330 1335	
gga aga cca act ata aaa aat gag aag ttt ttg gct ggt tta agt	4059
Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser	
1340 1345 1350	
act gac ggc ttc tgg gat att caa acc ttt aaa gtt att gaa gaa	4104
Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu	
1355 1360 1365	
gca gtt tat ttt cac cag cac agc att ctt gct tgt aaa att gaa	4149
Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu	
1370 1375 1380	
atg gtt gac tac aaa gaa gaa cat aat act aca ctg cca cag ttt	4194
Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe	
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